

# Joshua Schaaf

Oulu, Finland | [joshuaschaaf@gmail.com](mailto:joshuaschaaf@gmail.com) | 610-550-6432 | [github.com/viabard](https://github.com/viabard) | [linkedin.com/in/josh-schaaf](https://linkedin.com/in/josh-schaaf)  
[scholar.google.com](https://scholar.google.com) | [orcid.org/0009-0000-9745-4196](https://orcid.org/0009-0000-9745-4196) | Updated April 20th, 2026

## Education

---

- Oulu University**, Doctoral Researcher Aug 2025 – Current  
Oulu, Finland
- Temple University**, PSM (Professional Science Masters) in Bioinformatics ([Contact](#)) Sept 2020 – May 2022  
Philadelphia PA, USA
- GPA: 4.0/4.0
  - Machine Learning, Biostatistics, Biological Models in Python, Genomics
- Temple University**, BS in Biochemistry, Computer Science Minor Sept 2017 – May 2021  
Philadelphia PA, USA
- GPA: 3.88/4.0 *Magna Cum Laude*, With Distinction
  - Data Structures, Calculus, Organic Chemistry, Physical Chemistry, Biochemistry

## Language

---

**English** – Native | **Finnish** – Beginner | **Spanish** – Beginner

## Experience

---

- Bioinformatics Programmer Analyst II**, [HJF WHIRC](#) – Annandale, VA, USA January 2023 – July 2025  
Support bioinformatic efforts in a cancer proteomics laboratory: Early Career (Stage I)
- Develop, deploy, and publish **ProteoMixture**, a tool to determine relative abundance of tissue types from bulk High-Grade Serous Ovarian Cancer samples
  - Design and develop machine learning (ML) methods for classifying/regressing against patient clinical variables using multiomic data
  - Lead the development of computer vision-based tissue collection automation efforts
  - Develop and maintain statistical data analysis workflows for proteomic, transcriptomic, and clinical data levels for projects spanning multiple cancer types
  - Analyze peptide spectral match data from tandem mass tag (TMT) mass spectrometry experiments to generate comprehensive protein abundance reports
- Data Analyst**, [FOXO Technologies](#) – Remote – Davis CA, USA July 2021 – November 2022  
Developed tools to aid identification of epigenetic biomarkers.
- Developed, maintained, and tested **RAPA** (Robust Automated Parsimony Analysis), a Python package leveraging auto-ML platform Data Robot, to perform and plot intra-model recursive feature reduction
  - Created interactive dashboards for comparing clustering algorithms of methylation array data
- Undergraduate Genetic Researcher**, [Balciunas Lab](#) – Philadelphia PA, USA December 2018 – May 2021
- Created a genetically modified zebrafish to study the role of a transcription factor in cardiac tissue regeneration
  - Analyzed ChIP-seq data to identify binding locations/motifs of transcription factors in the zebrafish genome
- Undergraduate Biochemistry Researcher**, [Wang Group](#) – Philadelphia PA, USA May 2018 – September 2018
- Performed solid-phase peptide synthesis to generate antibody-drug conjugate linkers

## Publications

---

- ProteoMixture: A cell type deconvolution tool for bulk tissue proteomic data** March 2024  
iScience, Volume 27 (3)  
Authors: Pang-ning Teng, **Joshua Schaaf**, ... Nicholas W. Bateman  
DOI – [10.1016/j.isci.2024.109198](https://doi.org/10.1016/j.isci.2024.109198)

## Mapping three-dimensional intratumor proteomic heterogeneity in uterine serous carcinoma by multiregion microsampling

January 2024

Clinical proteomics, Volume 21 (1)

Authors: Allison L. Hunt, ... [Joshua Schaaf](#), ... Thomas P. Conrads

DOI – [10.1186/s12014-024-09451-2](https://doi.org/10.1186/s12014-024-09451-2)

## Presentations

---

Measuring Biochemistry with Lasers and Nanoparticles – [Poster](#)  
Progressing Towards a Label-Free Life-Cell Kinase Assay – [Oral](#)

[Science Day](#) – April 2026  
[LFTDays](#) – February 2026

Predicting Immune Cell Admixture in Bulk Proteomics Data Using ProteoMixture – [Poster](#)

[ASMS](#) – June 2025

- Session – Informatics: Algorithms and Statistical Advances

Evaluating the Performance of ProteoMixture, a Proteomics-Based Cell Deconvolution Tool in Pan-Cancer Data for > 1000 Patient Tumors – [Poster](#)

[ASMS](#) – June 2024

- Session – Informatics: Algorithms and Statistical Advances

Conditional Mutagenesis of Zebrafish *tcf21* – [Poster](#)

[TU URP Symposium](#) – 2019

- Undergraduate Research Program research symposium

## Awards and Honors

---

### Honors

- Temple University [Honors Program](#) (2018 – 2021)
- College of Science and Technology Dean's List (2017 – 2021)
- Latin Honors *Magna Cum Laude* (2021)
- Distinction in Major (2021)

### Awards

- [Science Scholars Program](#) (2019 – 2021)
- [Natan Luehrmann-Cowen Memorial Award](#) (2021)
- [Temple University Diamond Marching Band Scholarship](#) (2017 – 2018)
- Temple University Tuition Scholarship (2017 – 2021)

## Skills and Technologies

---

Python | R | Machine Learning (sklearn, pytorch, tensorflow, keras) | Data Visualization (seaborn, matplotlib, ggplot2) | Computer Vision | Proteomics | git | JavaScript | C | Linux | Mass Spectrometry

## Science Outreach and Communication

---

[Letters to a Pre-Scientist \(LPS\)](#)

September 2024 – Present

I am a pen-pal for a middle-school student from a school in a lower-income community. I help de-mystify science and scientists, and hopefully inspire my student to further consider a career that may have felt out of reach.